

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/448,868DATE: 12/14/1999
TIME: 16:43:39

INPUT SET: S34210.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2
3 (1) General Information:
4
5 (i) APPLICANT: Ni, Jian
6 Rosen, Craig A.
7 Pan, James G.
8 Gentz, Reiner L.
9 Dixit, Vishva M.
10
11 (ii) TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
12 Receptor 4), Member of the TNF-Receptor
13 Superfamily and Binding to Trail (AP02-L)
14
15 (iii) NUMBER OF SEQUENCES: 12
16
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
19 (B) STREET: 9410 KEY WEST AVENUE
20 (C) CITY: ROCKVILLE
21 (D) STATE: MD
22 (E) COUNTRY: US
23 (F) ZIP: 20850
24
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: Floppy disk
27 (B) COMPUTER: IBM PC compatible
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
30
31 (vi) CURRENT APPLICATION DATA:
32 (A) APPLICATION NUMBER: TO BE ASSIGNED
33 (B) FILING DATE: HERewith
34 (C) CLASSIFICATION:
35
36 (vi) PRIOR APPLICATION DATA:
37 (A) APPLICATION NUMBER: 09/013,895
38 (B) FILING DATE: 27-JAN-1998
39 (C) CLASSIFICATION:
40
41 (viii) ATTORNEY/AGENT INFORMATION:
42 (A) NAME: STEFFE, ERIC K.
43 (B) REGISTRATION NUMBER: 36,688
44 (C) REFERENCE/DOCKET NUMBER: 1488.1300004
45
46 (ix) TELECOMMUNICATION INFORMATION:

RAW SEQUENCE LISTING PATENT APPLICATION US/09/448,868

 DATE: 12/14/1999
 TIME: 16:43:39

INPUT SET: S34210.raw

 47 (A) TELEPHONE: (202) 371-2600
 48 (B) TELEFAX: (202) 371-2540
 49
 50

 51 (2) INFORMATION FOR SEQ ID NO:1:
 52

 53 (i) SEQUENCE CHARACTERISTICS:
 54 (A) LENGTH: 2152 base pairs
 55 (B) TYPE: nucleic acid
 56 (C) STRANDEDNESS: single
 57 (D) TOPOLOGY: linear
 58

 59 (ii) MOLECULE TYPE: DNA (genomic)
 60
 61

 62 (ix) FEATURE:
 63 (A) NAME/KEY: CDS
 64 (B) LOCATION: 19..1422
 65
 66
 67

 68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 69

70	TTCGGGCACG AGGGCAGG ATG GCG CCA CCA CCA GCT AGA GTA CAT CTA GGT	51
71	Met Ala Pro Pro Pro Ala Arg Val His Leu Gly	
72	1 5 10	
73		
74	GCG TTC CTG GCA GTG ACT CCG AAT CCC GGG AGC GCA GCG AGT GGG ACA	99
75	Ala Phe Leu Ala Val Thr Pro Asn Pro Gly Ser Ala Ala Ser Gly Thr	
76	15 20 25	
77		
78	GAG GCA GCC GCG GCC ACA CCC AGC AAA GTG TGG GGC TCT TCC GCG GGG	147
79	Glu Ala Ala Ala Ala Thr Pro Ser Lys Val Trp Gly Ser Ser Ala Gly	
80	30 35 40	
81		
82	AGG ATT GAA CCA CGA GGC GGG GGC CGA GGA GCG CTC CCT ACC TCC ATG	195
83	Arg Ile Glu Pro Arg Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser Met	
84	45 50 55	
85		
86	GGA CAG CAC GGA CCC AGT GCC CGG GCC CGG GCA GGG CGC GCC CCA GGA	243
87	Gly Gln His Gly Pro Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly	
88	60 65 70 75	
89		
90	CCC AGG CCG GCG CGG GAA GCC AGC CCT CGG CTC CGG GTC CAC AAG ACC	291
91	Pro Arg Pro Ala Arg Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr	
92	80 85 90	
93		
94	TTC AAG TTT GTC GTC GTC GGG GTC CTG CTG CAG GTC GTA CCT AGC TCA	339
95	Phe Lys Phe Val Val Val Gly Val Leu Leu Gln Val Val Pro Ser Ser	
96	95 100 105	
97		
98	GCT GCA ACC ATC AAA CTT CAT GAT CAA TCA ATT GGC ACA CAG CAA TGG	387
99	Ala Ala Thr Ile Lys Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp	

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100	110	115	120	
101				
102	GAA CAT AGC CCT TTG GGA GAG TTG TGT CCA CCA GGA TCT CAT AGA TCA			435
103	Glu His Ser Pro Leu Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser			
104	125	130	135	
105				
106	GAA CGT CCT GGA GCC TGT AAC CGG TGC ACA GAG GGT GTG GGT TAC ACC			483
107	Glu Arg Pro Gly Ala Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr			
108	140	145	150	155
109				
110	AAT GCT TCC AAC AAT TTG TTT GCT TGC CTC CCA TGT ACA GCT TGT AAA			531
111	Asn Ala Ser Asn Asn Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys Lys			
112		160	165	170
113				
114	TCA GAT GAA GAA GAG AGA AGT CCC TGC ACC ACG ACC AGG AAC ACA GCA			579
115	Ser Asp Glu Glu Glu Arg Ser Pro Cys Thr Thr Thr Arg Asn Thr Ala			
116		175	180	185
117				
118	TGT CAG TGC AAA CCA GGA ACT TTC CGG AAT GAC AAT TCT GCT GAG ATG			627
119	Cys Gln Cys Lys Pro Gly Thr Phe Arg Asn Asp Asn Ser Ala Glu Met			
120	190	195	200	
121				
122	TGC CGG AAG TGC AGC ACA GGG TGC CCC AGA GGG ATG GTC AAG GTC AAG			675
123	Cys Arg Lys Cys Ser Thr Gly Cys Pro Arg Gly Met Val Lys Val Lys			
124	205	210	215	
125				
126	GAT TGT ACG CCC TGG AGT GAC ATC GAG TGT GTC CAC AAA GAA TCA GGC			723
127	Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly			
128	220	225	230	235
129				
130	AAT GGA CAT AAT ATA TGG GTG ATT TTG GTT GTG ACT TTG GTT GTT CCG			771
131	Asn Gly His Asn Ile Trp Val Ile Leu Val Val Thr Leu Val Val Pro			
132		240	245	250
133				
134	TTG CTG TTG GTG GCT GTG CTG ATT GTC TGT TGT TGC ATC GGC TCA GGT			819
135	Leu Leu Leu Val Ala Val Leu Ile Val Cys Cys Cys Ile Gly Ser Gly			
136		255	260	265
137				
138	TGT GGA GGG GAC CCC AAG TGC ATG GAC AGG GTG TGT TTC TGG CGC TTG			867
139	Cys Gly Gly Asp Pro Lys Cys Met Asp Arg Val Cys Phe Trp Arg Leu			
140		270	275	280
141				
142	GGT CTC CTA CGA GGG CCT GGG GCT GAG GAC AAT GCT CAC AAC GAG ATT			915
143	Gly Leu Leu Arg Gly Pro Gly Ala Glu Asp Asn Ala His Asn Glu Ile			
144	285	290	295	
145				
146	CTG AGC AAC GCA GAC TCG CTG TCC ACT TTC GTC TCT GAG CAG CAA ATG			963
147	Leu Ser Asn Ala Asp Ser Leu Ser Thr Phe Val Ser Glu Gln Gln Met			
148	300	305	310	315
149				
150	GAA AGC CAG GAG CCG GCA GAT TTG ACA GGT GTC ACT GTA CAG TCC CCA			1011
151	Glu Ser Gln Glu Pro Ala Asp Leu Thr Gly Val Thr Val Gln Ser Pro			
152		320	325	330

153																	
154	GGG	GAG	GCA	CAG	TGT	CTG	CTG	GGA	CCG	GCA	GAA	GCT	GAA	GGG	TCT	CAG	1059
155	Gly	Glu	Ala	Gln	Cys	Leu	Leu	Gly	Pro	Ala	Glu	Ala	Glu	Gly	Ser	Gln	
156				335					340					345			
157																	
158	AGG	AGG	AGG	CTG	CTG	GTT	CCA	GCA	AAT	GGT	GCT	GAC	CCC	ACT	GAG	ACT	1107
159	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	Gly	Ala	Asp	Pro	Thr	Glu	Thr	
160			350					355					360				
161																	
162	CTG	ATG	CTG	TTC	TTT	GAC	AAG	TTT	GCA	AAC	ATC	GTG	CCC	TTT	GAC	TCC	1155
163	Leu	Met	Leu	Phe	Phe	Asp	Lys	Phe	Ala	Asn	Ile	Val	Pro	Phe	Asp	Ser	
164		365					370					375					
165																	
166	TGG	GAC	CAG	CTC	ATG	AGG	CAG	CTG	GAC	CTC	ACG	AAA	AAT	GAG	ATC	GAT	1203
167	Trp	Asp	Gln	Leu	Met	Arg	Gln	Leu	Asp	Leu	Thr	Lys	Asn	Glu	Ile	Asp	
168	380					385					390					395	
169																	
170	GTG	GTC	AGA	GCT	GGT	ACA	GCA	GGC	CCA	GGG	GAT	GCC	TTG	TAT	GCA	ATG	1251
171	Val	Val	Arg	Ala	Gly	Thr	Ala	Gly	Pro	Gly	Asp	Ala	Leu	Tyr	Ala	Met	
172					400					405					410		
173																	
174	CTG	ATG	AAA	TGG	GTC	AAC	AAA	ACT	GGA	CGG	AAC	GCC	TCG	ATC	CAC	ACC	1299
175	Leu	Met	Lys	Trp	Val	Asn	Lys	Thr	Gly	Arg	Asn	Ala	Ser	Ile	His	Thr	
176				415					420					425			
177																	
178	CTG	CTG	GAT	GCC	TTG	GAG	AGG	ATG	GAA	GAG	AGA	CAT	GCA	AAA	GAG	AAG	1347
179	Leu	Leu	Asp	Ala	Leu	Glu	Arg	Met	Glu	Glu	Arg	His	Ala	Lys	Glu	Lys	
180			430					435					440				
181																	
182	ATT	CAG	GAC	CTC	TTG	GTG	GAC	TCT	GGA	AAG	TTC	ATC	TAC	TTA	GAA	GAT	1395
183	Ile	Gln	Asp	Leu	Leu	Val	Asp	Ser	Gly	Lys	Phe	Ile	Tyr	Leu	Glu	Asp	
184		445						450					455				
185																	
186	GGC	ACA	GGC	TCT	GCC	GTG	TCC	TTG	GAG	TGAAAGACTC TTTTACCAG							1442
187	Gly	Thr	Gly	Ser	Ala	Val	Ser	Leu	Glu								
188	460					465											
189																	
190	AGGTTTCCTC			TTAGGTGTTA			GGAGTTAATA			CATATTAGGT			TTTTTTTTTT				

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206 TCATGGTGGT CAATTGGAGG TGTTAATTTG AATGGATTAA GGAACACCTA GAACACTGGT 1982
 207
 208 AAGGCATTAT TTCTGGGACA TTATTTCTGG GCATGTCTTC GAGGGTGTTT CCAGAGGGGA 2042
 209
 210 TTGGCATGCG ATCGGGTGGA CTGAGTGGAA AAGACCTACC CTTAATTTGG GGGGGCACCG 2102
 211
 212 TCCGACAGAC TGGGGAGCAA GATAGAAGAA AACAAAAAAA AAAAAAAAAA 2152
 213
 214

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

225
 226 Met Ala Pro Pro Pro Ala Arg Val His Leu Gly Ala Phe Leu Ala Val
 227 1 5 10 15
 228
 229 Thr Pro Asn Pro Gly Ser Ala Ala Ser Gly Thr Glu Ala Ala Ala Ala
 230 20 25 30
 231
 232 Thr Pro Ser Lys Val Trp Gly Ser Ser Ala Gly Arg Ile Glu Pro Arg
 233 35 40 45
 234
 235 Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro
 236 50 55 60
 237
 238 Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly Pro Arg Pro Ala Arg
 239 65 70 75 80
 240
 241 Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr Phe Lys Phe Val Val
 242 85 90 95
 243
 244 Val Gly Val Leu Leu Gln Val Val Pro Ser Ser Ala Ala Thr Ile Lys
 245 100 105 110
 246
 247 Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His Ser Pro Leu
 248 115 120 125
 249
 250 Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu Arg Pro Gly Ala
 251 130 135 140
 252
 253 Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr Asn Ala Ser Asn Asn
 254 145 150 155 160
 255
 256 Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys Lys Ser Asp Glu Glu Glu
 257 165 170 175
 258

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/448,868DATE: 12/14/1999
TIME: 16:43:41

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***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

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52

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 2152 base pairs

55 (B) TYPE: nucleic acid

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68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

69

70 TTCGGGCACG AGGGCAGG ATG GCG CCA CCA CCA GCT AGA GTA CAT CTA GGT 51

71 Met Ala Pro Pro Pro Ala Arg Val His Leu Gly

72 1 5 10

73

74 GCG TTC CTG GCA GTG ACT CCG AAT CCC GGG AGC GCA GCG AGT GGG ACA 99

75 Ala Phe Leu Ala Val Thr Pro Asn Pro Gly Ser Ala Ala Ser Gly Thr

76 15 20 25

77

78 GAG GCA GCC GCG GCC ACA CCC AGC AAA GTG TGG GGC TCT TCC GCG GGG 147

79 Glu Ala Ala Ala Ala Thr Pro Ser Lys Val Trp Gly Ser Ser Ala Gly

80 30 35 40

81

82 AGG ATT GAA CCA CGA GGC GGG GGC CGA GGA GCG CTC CCT ACC TCC ATG 195

83 Arg Ile Glu Pro Arg Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser Met

84 45 50 55

85

86 GGA CAG CAC GGA CCC AGT GCC CGG GCC CGG GCA GGG CGC GCC CCA GGA 243

87 Gly Gln His Gly Pro Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly

88 60 65 70 75

89

90 CCC AGG CCG GCG CGG GAA GCC AGC CCT CGG CTC CGG GTC CAC AAG ACC 291

91 Pro Arg Pro Ala Arg Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr

92 80 85 90

93

94 TTC AAG TTT GTC GTC GTC GGG GTC CTG CTG CAG GTC GTA CCT AGC TCA 339

95 Phe Lys Phe Val Val Val Gly Val Leu Leu Gln Val Val Pro Ser Ser

96 95 100 105

97

RAW SEQUENCE LISTING PATENT APPLICATION US/09/448,868

 DATE: 12/14/1999
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98	GCT	GCA	ACC	ATC	AAA	CTT	CAT	GAT	CAA	TCA	ATT	GGC	ACA	CAG	CAA	TGG	387
99	Ala	Ala	Thr	Ile	Lys	Leu	His	Asp	Gln	Ser	Ile	Gly	Thr	Gln	Gln	Trp	
100			110					115					120				
101																	
102	GAA	CAT	AGC	CCT	TTG	GGA	GAG	TTG	TGT	CCA	CCA	GGA	TCT	CAT	AGA	TCA	435
103	Glu	His	Ser	Pro	Leu	Gly	Glu	Leu	Cys	Pro	Pro	Gly	Ser	His	Arg	Ser	
104		125					130					135					
105																	
106	GAA	CGT	CCT	GGA	GCC	TGT	AAC	CGG	TGC	ACA	GAG	GGT	GTG	GGT	TAC	ACC	483
107	Glu	Arg	Pro	Gly	Ala	Cys	Asn	Arg	Cys	Thr	Glu	Gly	Val	Gly	Tyr	Thr	
108	140					145					150					155	
109																	
110	AAT	GCT	TCC	AAC	AAT	TTG	TTT	GCT	TGC	CTC	CCA	TGT	ACA	GCT	TGT	AAA	531
111	Asn	Ala	Ser	Asn	Asn	Leu	Phe	Ala	Cys	Leu	Pro	Cys	Thr	Ala	Cys	Lys	
112				160					165						170		
113																	
114	TCA	GAT	GAA	GAA	GAG	AGA	AGT	CCC	TGC	ACC	ACG	ACC	AGG	AAC	ACA	GCA	579
115	Ser	Asp	Glu	Glu	Glu	Arg	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr	Ala	
116			175					180					185				
117																	
118	TGT	CAG	TGC	AAA	CCA	GGA	ACT	TTC	CGG	AAT	GAC	AAT	TCT	GCT	GAG	ATG	627
119	Cys	Gln	Cys	Lys	Pro	Gly	Thr	Phe	Arg	Asn	Asp	Asn	Ser	Ala	Glu	Met	
120		190					195					200					
121																	
122	TGC	CGG	AAG	TGC	AGC	ACA	GGG	TGC	CCC	AGA	GGG	ATG	GTC	AAG	GTC	AAG	675
123	Cys	Arg	Lys	Cys	Ser	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val	Lys	Val	Lys	
124		205				210					215						
125																	
126	GAT	TGT	ACG	CCC	TGG	AGT	GAC	ATC	GAG	TGT	GTC	CAC	AAA	GAA	TCA	GGC	723
127	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	Lys	Glu	Ser	Gly	
128	220				225				230				235				
129																	
130	AAT	GGA	CAT	AAT	ATA	TGG	GTG	ATT	TTG	GTT	GTG	ACT	TTG	GTT	GTT	CCG	771
131	Asn	Gly	His	Asn	Ile	Trp	Val	Ile	Leu	Val	Val	Thr	Leu	Val	Val	Pro	
132				240				245					250				
133																	
134	TTG	CTG	TTG	GTG	GCT	GTG	CTG	ATT	GTC	TGT	TGT	TGC	ATC	GGC	TCA	GGT	819
135	Leu	Leu	Leu	Val	Ala	Val	Leu	Ile	Val	Cys	Cys	Cys	Ile	Gly	Ser	Gly	
136			255				260					265					
137																	
138	TGT	GGA	GGG	GAC	CCC	AAG	TGC	ATG	GAC	AGG	GTG	TGT	TTC	TGG	CGC	TTG	867
139	Cys	Gly	Gly	Asp	Pro	Lys	Cys	Met	Asp	Arg	Val	Cys	Phe	Trp	Arg	Leu	
140		270				275					280						
141																	
142	GGT	CTC	CTA	CGA	GGG	CCT	GGG	GCT	GAG	GAC	AAT	GCT	CAC	AAC	GAG	ATT	915
143	Gly	Leu	Leu	Arg	Gly	Pro	Gly	Ala	Glu	Asp	Asn	Ala	His	Asn	Glu	Ile	
144		285			290			295									
145																	
146	CTG	AGC	AAC	GCA	GAC	TCG	CTG	TCC	ACT	TTC	GTC	TCT	GAG	CAG	CAA	ATG	963
147	Leu	Ser	Asn	Ala	Asp	Ser	Leu	Ser	Thr	Phe	Val	Ser	Glu	Gln	Gln	Met	
148	300				305			310					315				
149																	
150	GAA	AGC	CAG	GAG	CCG	GCA	GAT	TTG	ACA	GGT	GTC	ACT	GTA	CAG	TCC	CCA	1011

RAW SEQUENCE LISTING PATENT APPLICATION US/09/448,868

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151	Glu Ser Gln Glu Pro Ala Asp Leu Thr Gly Val Thr Val Gln Ser Pro	
152	320 325 330	
153		
154	GGG GAG GCA CAG TGT CTG CTG GGA CCG GCA GAA GCT GAA GGG TCT CAG	1059
155	Gly Glu Ala Gln Cys Leu Leu Gly Pro Ala Glu Ala Glu Gly Ser Gln	
156	335 340 345	
157		
158	AGG AGG AGG CTG CTG GTT CCA GCA AAT GGT GCT GAC CCC ACT GAG ACT	1107
159	Arg Arg Arg Leu Leu Val Pro Ala Asn Gly Ala Asp Pro Thr Glu Thr	
160	350 355 360	
161		
162	CTG ATG CTG TTC TTT GAC AAG TTT GCA AAC ATC GTG CCC TTT GAC TCC	1155
163	Leu Met Leu Phe Phe Asp Lys Phe Ala Asn Ile Val Pro Phe Asp Ser	
164	365 370 375	
165		
166	TGG GAC CAG CTC ATG AGG CAG CTG GAC CTC ACG AAA AAT GAG ATC GAT	1203
167	Trp Asp Gln Leu Met Arg Gln Leu Asp Leu Thr Lys Asn Glu Ile Asp	
168	380 385 390 395	
169		
170	GTG GTC AGA GCT GGT ACA GCA GGC CCA GGG GAT GCC TTG TAT GCA ATG	1251
171	Val Val Arg Ala Gly Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala Met	
172	400 405 410	
173		
174	CTG ATG AAA TGG GTC AAC AAA ACT GGA CGG AAC GCC TCG ATC CAC ACC	1299
175	Leu Met Lys Trp Val Asn Lys Thr Gly Arg Asn Ala Ser Ile His Thr	
176	415 420 425	
177		
178	CTG CTG GAT GCC TTG GAG AGG ATG GAA GAG AGA CAT GCA AAA GAG AAG	1347
179	Leu Leu Asp Ala Leu Glu Arg Met Glu Glu Arg His Ala Lys Glu Lys	
180	430 435 440	
181		
182	ATT CAG GAC CTC TTG GTG GAC TCT GGA AAG TTC ATC TAC TTA GAA GAT	1395
183	Ile Gln Asp Leu Leu Val Asp Ser Gly Lys Phe Ile Tyr Leu Glu Asp	
184	445 450 455	
185		
186	GGC ACA GGC TCT GCC GTG TCC TTG GAG TGAAAGACTC TTTTACCAG	1442
187	Gly Thr Gly Ser Ala Val Ser Leu Glu	
188	460 465	
189		
190	AGGTTTCCTC TTAGGTGTTA GGAGTTAATA CATATTAGGT TTTTTTTTTT TTTAACATGT	1502
191		
192	ATACAAAGTA AATTCTTAGC CACGTGTATT GGCTCCTGCC TGTAATCCCA TCACTTTGGG	1562
193		
194	AGGCTGACGC CGGTGGATCC ACTTGAGGTC CGAAGTTCCA AGACCAGCCC TGAACCAACA	1622
195		
196	TCGTGGAAAT GCCCGTCTTT TACAAAAAAA TACCAAAAAT TCAACTGGAA TGTGCATGGT	1682
197		
198	GTGTGCCATC ATTTCTTCGG CTAACCTACGG GAGGTCTGAG GCCAGGAGAA TCCACTTGAA	1742
199		
200	CCCCACGAAG GACAGTGTAG ACTGCAGATT GCACCACTGC ACTCCCAGCC TGGGAACACA	1802
201		
202	GAGCAAGACT CTGTCTCAAG ATAAAATAAA ATAAACTTGA AAGAATTATT GCCCGACTGA	1862
203		

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PATENT APPLICATION US/09/448,868DATE: 12/14/1999
TIME: 16:43:42*INPUT SET: S34210.raw*

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205		
206	TCATGGTGGT CAATTGGAGG TGTTAATTG AATGGATTAA GGAACACCTA GAACACTGGT	1982
207		
208	AAGGCATTAT TTCTGGGACA TTATTTCTGG GCATGTCTTC GAGGGTGTTT CCAGAGGGGA	2042
209		
210	TTGGCATGCG ATCGGGTGGA CTGAGTGGAA AAGACCTACC CTTAATTTGG GGGGGCACCG	2102
211		
212	TCCGACAGAC TGGGGAGCAA GATAGAAGAA AACAAAAAAA AAAAAAAAAA	2152
213		
214		

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/448,868

DATE: 12/14/1999
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Line	Error	Original Text
32	Wrong application Serial Number	(A) APPLICATION NUMBER: TO BE ASSIGNED

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/448,868

DATE: 12/14/1999
TIME: 04:37:43

INPUT SET: S34210.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

SEQUENCE LISTING

(1) General Information:

Does Not Comply
Corrected Diskette Needed

(i) APPLICANT: Ni, Jian
Rosen, Craig A.
Pan, James G.
Gentz, Reiner L.
Dixit, Vishva M.

(ii) TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
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Superfamily and Binding to Trail (AP02-L)

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(E) COUNTRY: US
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: HERewith
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/013,895
(B) FILING DATE: 27-JAN-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: STEFFE, ERIC K.
(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1488.1300004

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/448,868DATE: 12/14/1999
TIME: 04:37:43

INPUT SET: S34210.raw

46 (ix) TELECOMMUNICATION INFORMATION:
47 (A) TELEPHONE: (202) 371-2600
48 (B) TELEFAX: (202) 371-2540
49
50

ERRORED SEQUENCES FOLLOW:

51 (2) INFORMATION FOR SEQ ID NO:1:
52
53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 2152 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58
59 (ii) MOLECULE TYPE: DNA (genomic)
60
61
62 (ix) FEATURE:
63 (A) NAME/KEY: CDS
64 (B) LOCATION: 19..1422
65
66
67
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

69
70 TTCGGGCACG AGGGCAGG ATG GCG CCA CCA CCA GCT AGA GTA CAT CTA GGT
71 51
72 Met Ala Pro Pro Pro Ala Arg Val His Leu Gly
73 1 5 10
74
75 GCG TTC CTG GCA GTG ACT CCG AAT CCC GGG AGC GCA GCG AGT GGG ACA 99
76 Ala Phe Leu Ala Val Thr Pro Asn Pro Gly Ser Ala Ala Ser Gly Thr
77 15 20 25
78
79 GAG GCA GCC GCG GCC ACA CCC AGC AAA GTG TGG GGC TCT TCC GCG GGG 147
80 Glu Ala Ala Ala Ala Thr Pro Ser Lys Val Trp Gly Ser Ser Ala Gly
81 30 35 40
82
83 AGG ATT GAA CCA CGA GGC GGG GGC CGA GGA GCG CTC CCT ACC TCC ATG 195
84 Arg Ile Glu Pro Arg Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser Met
85 45 50 55
86
87 GGA CAG CAC GGA CCC AGT GCC CGG GCC CGG GCA GGG CGC GCC CCA GGA 243
88 Gly Gln His Gly Pro Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly
89 60 65 70 75
90
91 CCC AGG CCG GCG CGG GAA GCC AGC CCT CGG CTC CGG GTC CAC AAG ACC 291
92 Pro Arg Pro Ala Arg Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr

RAW SEQUENCE LISTING PATENT APPLICATION US/09/448,868

DATE: 12/14/1999
TIME: 04:37:43

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	80	85	90	
93				
94				
95	TTC AAG TTT GTC GTC GTC GGG GTC CTG CTG CAG GTC GTA CCT AGC TCA			339
96	Phe Lys Phe Val Val Val Gly Val Leu Leu Gln Val Val Pro Ser Ser			
97		95	100	105
98				
99	GCT GCA ACC ATC AAA CTT CAT GAT CAA TCA ATT GGC ACA CAG CAA TGG			387
100	Ala Ala Thr Ile Lys Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp			
101		110	115	120
102				
103	GAA CAT AGC CCT TTG GGA GAG TTG TGT CCA CCA GGA TCT CAT AGA TCA			435
104	Glu His Ser Pro Leu Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser			
105		125	130	135
106				
107	GAA CGT CCT GGA GCC TGT AAC CGG TGC ACA GAG GGT GTG GGT TAC ACC			483
108	Glu Arg Pro Gly Ala Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr			
109	140	145	150	155
110				
111	AAT GCT TCC AAC AAT TTG TTT GCT TGC CTC CCA TGT ACA GCT TGT AAA			531
112	Asn Ala Ser Asn Asn Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys Lys			
113		160	165	170
114				
115	TCA GAT GAA GAA GAG AGA AGT CCC TGC ACC ACG ACC AGG AAC ACA GCA			579
116	Ser Asp Glu Glu Glu Arg Ser Pro Cys Thr Thr Thr Arg Asn Thr Ala			
117		175	180	185
118				
119	TGT CAG TGC AAA CCA GGA ACT TTC CGG AAT GAC AAT TCT GCT GAG ATG			627
120	Cys Gln Cys Lys Pro Gly Thr Phe Arg Asn Asp Asn Ser Ala Glu Met			
121		190	195	200
122				
123	TGC CGG AAG TGC AGC ACA GGG TGC CCC AGA GGG ATG GTC AAG GTC AAG			675
124	Cys Arg Lys Cys Ser Thr Gly Cys Pro Arg Gly Met Val Lys Val Lys			
125		205	210	215
126				
127	GAT TGT ACG CCC TGG AGT GAC ATC GAG TGT GTC CAC AAA GAA TCA GGC			723
128	Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly			
129	220	225	230	235
130				
131	AAT GGA CAT AAT ATA TGG GTG ATT TTG GTT GTG ACT TTG GTT GTT CCG			771
132	Asn Gly His Asn Ile Trp Val Ile Leu Val Val Thr Leu Val Val Pro			
133		240	245	250
134				
135	TTG CTG TTG GTG GCT GTG CTG ATT GTC TGT TGT TGC ATC GGC TCA GGT			819
136	Leu Leu Leu Val Ala Val Leu Ile Val Cys Cys Cys Ile Gly Ser Gly			
137		255	260	265
138				
139	TGT GGA GGG GAC CCC AAG TGC ATG GAC AGG GTG TGT TTC TGG CGC TTG			867
140	Cys Gly Gly Asp Pro Lys Cys Met Asp Arg Val Cys Phe Trp Arg Leu			
141		270	275	280
142				
143	GGT CTC CTA CGA GGG CCT GGG GCT GAG GAC AAT GCT CAC AAC GAG ATT			915
144	Gly Leu Leu Arg Gly Pro Gly Ala Glu Asp Asn Ala His Asn Glu Ile			
145		285	290	295

INPUT SET: S34210.raw

146																			
147	CTG	AGC	AAC	GCA	GAC	TCG	CTG	TCC	ACT	TTC	GTC	TCT	GAG	CAG	CAA	ATG			963
148	Leu	Ser	Asn	Ala	Asp	Ser	Leu	Ser	Thr	Phe	Val	Ser	Glu	Gln	Gln	Met			
149	300																		315
150																			
151	GAA	AGC	CAG	GAG	CCG	GCA	GAT	TTG	ACA	GGT	GTC	ACT	GTA	CAG	TCC	CCA			1011
152	Glu	Ser	Gln	Glu	Pro	Ala	Asp	Leu	Thr	Gly	Val	Thr	Val	Gln	Ser	Pro			
153					320						325					330			
154																			
155	GGG	GAG	GCA	CAG	TGT	CTG	CTG	GGA	CCG	GCA	GAA	GCT	GAA	GGG	TCT	CAG			1059
156	Gly	Glu	Ala	Gln	Cys	Leu	Leu	Gly	Pro	Ala	Glu	Ala	Glu	Gly	Ser	Gln			
157				335					340						345				
158																			
159	AGG	AGG	AGG	CTG	CTG	GTT	CCA	GCA	AAT	GGT	GCT	GAC	CCC	ACT	GAG	ACT			1107
160	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	Gly	Ala	Asp	Pro	Thr	Glu	Thr			
161			350						355					360					
162																			
163	CTG	ATG	CTG	TTC	TTT	GAC	AAG	TTT	GCA	AAC	ATC	GTG	CCC	TTT	GAC	TCC			1155
164	Leu	Met	Leu	Phe	Phe	Asp	Lys	Phe	Ala	Asn	Ile	Val	Pro	Phe	Asp	Ser			
165		365						370					375						
166																			
167	TGG	GAC	CAG	CTC	ATG	AGG	CAG	CTG	GAC	CTC	ACG	AAA	AAT	GAG	ATC	GAT			1203
168	Trp	Asp	Gln	Leu	Met	Arg	Gln	Leu	Asp	Leu	Thr	Lys	Asn	Glu	Ile	Asp			
169	380					385						390				395			
170																			
171	GTG	GTC	AGA	GCT	GGT	ACA	GCA	GGC	CCA	GGG	GAT	GCC	TTG	TAT	GCA	ATG			1251
172	Val	Val	Arg	Ala	Gly	Thr	Ala	Gly	Pro	Gly	Asp	Ala	Leu	Tyr	Ala	Met			
173					400						405					410			
174																			
175	CTG	ATG	AAA	TGG	GTC	AAC	AAA	ACT	GGA	CGG	AAC	GCC	TCG	ATC	CAC	ACC			1299
176	Leu	Met	Lys	Trp	Val	Asn	Lys	Thr	Gly	Arg	Asn	Ala	Ser	Ile	His	Thr			
177				415						420					425				
178																			
179	CTG	CTG	GAT	GCC	TTG	GAG	AGG	ATG	GAA	GAG	AGA	CAT	GCA	AAA	GAG	AAG			
180	1347																		
181	Leu	Leu	Asp	Ala	Leu	Glu	Arg	Met	Glu	Glu	Arg	His	Ala	Lys	Glu	Lys			
182			430						435										

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/448,868DATE: 12/14/1999
TIME: 04:37:44

INPUT SET: S34210.raw

--> 199 TGAACCAACA 1622
200
201 TCGTGGAAT GCCCGTCTTT TACAAAAAA TACCAAAAT TCAACTGGAA
--> 202 TGTGCATGGT 1682
203
204 GTGTGCCATC ATTTCTCTCGG CTAACCTACGG GAGGTCTGAG GCCAGGAGAA
--> 205 TCCACTTGAA 1742
206
207 CCCACGAAG GACAGTGTAG ACTGCAGATT GCACCACTGC ACTCCCAGCC
--> 208 TGGGAACACA 1802
209
210 GAGCAAGACT CTGTCTCAAG ATAAAATAAA ATAACTTGA AAGAATTATT
--> 211 GCCCGACTGA 1862
212
213 GGCTCACATG CCAAAGGAAA ATCTGGTTCT CCCCTGAGCT GGCCTCCGTG
--> 214 TGTTTCCTTA 1922
215
216 TCATGGTGGT CAATTGGAGG TGTTAATTG AATGGATTAA GGAACACCTA
--> 217 GAACACTGGT 1982
218
219 AAGGCATTAT TTCTGGGACA TTATTTCTGG GCATGTCTTC GAGGGTGTTT
--> 220 CCAGAGGGGA 2042
221
222 TTGGCATGCG ATCGGGTGGA CTGAGTGGA AAGACCTACC CTTAATTG
--> 223 GGGGGCACCG 2102
224
225 TCCGACAGAC TGGGGAGCAA GATAGAAGAA AACAAAAAA AAAAAAA
226 2152
227
228

*same
env*

831 (2) INFORMATION FOR SEQ ID NO:6:
832
833 (i) SEQUENCE CHARACTERISTICS:
--> 834 (A) LENGTH: 426 base pairs
835 (B) TYPE: nucleic acid
836 (C) STRANDEDNESS: single
837 (D) TOPOLOGY: linear
838
839 (ii) MOLECULE TYPE: DNA (genomic)
840
841
842
843
844 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
845
846 GGCANAGGTN CGTACCTAGC TCACCTGCAA CCATCAAAT TNATGATCAA
--> 847 TCAATTGGCA 60
848
849 CACAGCAATG GGAAACATAG CCCTTTGGAA GANTTGTNTC CACCAGGATC
--> 850 TCATAGATCA 120
851
852 AACATCCTG GGAGCCTGTT AACCGGTGCC CCAAAGGNTG GTCAAGGTCA

same

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/448,868DATE: 12/14/1999
TIME: 04:37:44

INPUT SET: S34210.raw

--> 853 AGGAATTGTT 180
854
855 NCGCCCTGGA AGTGAACATC GAGTGTNTCC ACAAAGGATT CAGGCAATGG
--> 856 GACATAAATA 240
857
858 TATGGGTGAA TTTTGGTTGT GAACTTTGGT TGNTCCCGTT GNTGTTGNTG
--> 859 GCTGTGCTGA 300
860
861 TTGTTTGTTG TTGCATCGGC TTCAGGTTNT GGAGGGGGAC CCAAGTGCAT
--> 862 GGACAGGGTG 360
863
864 TGTTTCTGGG GTTTGGGTCT CTTAGAGGGC NTGGGTTANG GCANGTTCAC
--> 865 AAGGGTTTTA 420
866
867 GCAANG
868

426

869 (2) INFORMATION FOR SEQ ID NO:7:
870
871 (i) SEQUENCE CHARACTERISTICS:
--> 872 (A) LENGTH: 339 base pairs
873 (B) TYPE: nucleic acid
874 (C) STRANDEDNESS: single
875 (D) TOPOLOGY: linear
876
877 (ii) MOLECULE TYPE: DNA (genomic)
878
879
880
881
882 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
883
884 TGGGGCTGAG GACAATGCTG ACNACGAGAT TCTGAGCAAC GCAGNACTNG
--> 885 CTGTCCACTT 60
886
887 TCGTCTNTGN GCAGCAAATG GAAAGCCAGG AGCCGGCAGA TTTGACAGGT
--> 888 GTCACTGTAC 120
889
890 AGTCCCCAGG GGAGGCACAG TGTCTGCTGG TGAGTTGGGG ACAGGCCCTT
--> 891 GCAAGACCTT 180
892
893 GTGAGGCAGG GGGTGAAGGC CATGNCTCGG CTTCNNNTGG TCAAAGGGGA
--> 894 AGTGGAGCCT 240
895
896 GAGGGAGATG GGACTTNAGG GGGACGGNGC TCGGTGGGGA AAAAGCAGCC
--> 897 ACCNTTTGAC 300
898
899 AAGGGGGACA GGCATTTTTN CAAATGTGTG CTTNTTGGT
900

Done

339

943 (2) INFORMATION FOR SEQ ID NO:11:
944
945 (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/448,868DATE: 12/14/1999
TIME: 04:37:45

INPUT SET: S34210.raw

--> 946 (A) LENGTH: 29 base pairs
947 (B) TYPE: nucleic acid
948 (C) STRANDEDNESS: single
949 (D) TOPOLOGY: linear
950
951 (ii) MOLECULE TYPE: DNA (genomic)
952
953 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
954
955
956 29
957

GCGGGATCCT CAATTATGTC CATTGCCTG

958 (2) INFORMATION FOR SEQ ID NO:12:
959
960 (i) SEQUENCE CHARACTERISTICS:
--> 961 (A) LENGTH: 29 base pairs
962 (B) TYPE: nucleic acid
963 (C) STRANDEDNESS: single
964 (D) TOPOLOGY: linear
965
966 (ii) MOLECULE TYPE: DNA (genomic)
967
968 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
969
970
971 29
972
973
974
975
976

GCGAAGCTTT CAATTATGTC C

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/09/448,868

DATE: 12/14/1999
TIME: 04:37:45

INPUT SET: S34210.raw

Line	Error	Original Text
32	Wrong application Serial Number	(A) APPLICATION NUMBER: TO BE ASSIGNED
54	Entered (2152) and Calc. Seq. Length (1453) differ	(A) LENGTH: 2152 base pairs
75	# of Sequences for line conflicts w/ running total	GCG TTC CTG GCA GTG ACT CCG AAT CCC GGG AG
184	# of Sequences for line conflicts w/ running total	ATT CAG GAC CTC TTG GTG GAC TCT GGA AAG TT
193	# of Sequences for line conflicts w/ running total	TTTAACATGT 1502
196	# of Sequences for line conflicts w/ running total	TCACTTTGGG 1562
199	# of Sequences for line conflicts w/ running total	TGAACCAACA 1622
202	# of Sequences for line conflicts w/ running total	TGTGCATGGT 1682
205	# of Sequences for line conflicts w/ running total	TCCACTTGAA 1742
208	# of Sequences for line conflicts w/ running total	TGGGAACACA 1802
211	# of Sequences for line conflicts w/ running total	GCCCGACTGA 1862
214	# of Sequences for line conflicts w/ running total	TGTTTCCTTA 1922
217	# of Sequences for line conflicts w/ running total	GAACACTGGT 1982
220	# of Sequences for line conflicts w/ running total	CCAGAGGGGA 2042
223	# of Sequences for line conflicts w/ running total	GGGGGCACCG 2102
834	Entered (426) and Calc. Seq. Length (76) differ	(A) LENGTH: 426 base pairs
847	# of Sequences for line conflicts w/ running total	TCAATTGGCA 60
850	# of Sequences for line conflicts w/ running total	TCATAGATCA 120
853	# of Sequences for line conflicts w/ running total	AGGAATTGTT 180
856	# of Sequences for line conflicts w/ running total	GACATAAATA 240
859	# of Sequences for line conflicts w/ running total	GCTGTGCTGA 300
862	# of Sequences for line conflicts w/ running total	GGACAGGGTG 360
865	# of Sequences for line conflicts w/ running total	AAGGGTTTTA 420
872	Entered (339) and Calc. Seq. Length (89) differ	(A) LENGTH: 339 base pairs
885	# of Sequences for line conflicts w/ running total	CTGTCCACTT 60
888	# of Sequences for line conflicts w/ running total	GTCACGTAC 120
891	# of Sequences for line conflicts w/ running total	GCAAGACCTT 180
894	# of Sequences for line conflicts w/ running total	AGTGGAGCCT 240
897	# of Sequences for line conflicts w/ running total	ACCNTTTGAC 300
946	Entered (29) and Calc. Seq. Length (0) differ	(A) LENGTH: 29 base pairs
961	Entered (29) and Calc. Seq. Length (0) differ	(A) LENGTH: 29 base pairs